

QY 424 VDRNRNQVIAAGCGGGGUGLMLGLBLITVKLHQPLKAVFVNNSLGLGMVAKLEMVGEPEFGT 483

Db 425 TDERRQVVSMSGDFMMLGDFDFTLWHDLPVKTVLFNNNSLGLGVLELMVAGLPISHGV 484

QY 484 DHEEVNEFAEIAAAGIKSVRTPDKKVREQLAEALAYPGPVLIDIVDPNALISPTITW 543

Db 485 ANKNPPFAAAVEACGAFGVRYERPKPQLLAGAIKAARKRKGPAVLVDWVTDPNALISPTPK 544

QY 544 EQWMGFSKAATRTVFGGGVGAMIDLARSNTNRP 579

Db 545 DMVGFALASKVILDGGVGVRMLQMARSNLRRNP 580

F:50/Active site: Glu #status predicted

RESULT 2

DEFCPC

PY: Pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli

N; Alternate name: pyruvate oxidase

C; Species: Escherichia coli

C; Accession: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 05-Nov-1999

R; Grabau, C.; Cronan, Jr., J.E.

Nucleic Acids Res. 14, 5449-5460, 1986

A; Title: Nucleotide sequence and deduced amino acid sequence of Escherichia coli pyruvate

A; Reference number: A23648; MUID: 88286555

A; Accession: A23648

A; Molecule type: DNA

A; Residues: 1-572 <GRA>

A; Cross-references: GB:x04105; GB:M13947; GB:M13948; NID:942472; PIDN:CAA27725.1; PID:9426617

A; Experimental source: strain K-12; Shao, Y.

R; Lattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

Schiff, D.J.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A; Title: The complete genome sequence of Escherichia coli K-12.

A; Reference number: A64720; MUID:97426617

A; Status: nucleic acid sequence not shown; translation not shown

A; Residue type: DNA

A; Residues: 1-572 <BLAT>

A; Cross-references: GB:AE000188; GB:U00096; NID:91787084; PIDN:ACT73958.1; PID:91787096;

A; Experimental source: strain K-12, substrain MG1655

R; Grabau, C.; Chang, Y.Y.; Cronan, J.E.

J. Biol. Chem. 264, 12510-12519, 1989

A; Title: Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small altera

A; Reference number: 155291; MUID:89308683

A; Address: 155291

A; Status: translated from GB/EMBL/DBJ

A; Residues: 1-363, 'HE', 366-413, 'HCV', 417-572 <RES>

A; Experimental source: strain K-12; MUID:91009024; PIDN:AAB59101.1; PID:91009025

R; Chang, Y.Y.; Wang, A.Y.; Cronan, J.E.

Mol. Microbiol. 11, 1019-1028, 1994

A; Title: Expression of Escherichia coli pyruvate oxidase (PoxB) depends on the sigma fac

A; Reference number: 157556; MUID:94293772

A; Status: translated from GB/EMBL/DBJ

A; Molecule type: DNA

A; Residues: 1-22 <RES>

A; Cross-references: GB:s73268; NID:9658127; PIDN:AAB31180.1; PID:9685128

C; Comment: The sequence of this protein was shown to be homologous with those of the lar

ough, pyruvate is the end product. C; Comment: This protein is not to be confused with a similar enzyme, pyruvate (or pyruvi

C; Genetics: C; Complex: homotetramer

A; Map position: 19 min

C; Function:

A; Description: catalyzes the conversion of pyruvate to acetate and carbon dioxide in the

A; Note: in the presence of pyruvate and cofactor thiamine pyrophosphate, the addition of

C; Superfamily: acetylactate syntase large chain; thiamin pyrophosphate-binding domain

C; Keywords: FAD; flavoroprotein; homotetramer; lipid binding; magnesium; membrane protein; F:432-470/Domain: thiamin pyrophosphate-binding domain homology <TPB>

QY 60 SLTIGELAVQAAASCOPGNHLIQLCYSRFLRNGAKVLAQSIAQISTFFETHPRIL 119

Db 61 AOLSGELAVQAAASCOPGNHLIQLCYSRFLRNGAKVLAQSIAQISTFFETHPRIL 120

QY 120 FKCCSGICENVNGGQGERLTLHAIQSTWAGKGSVWVTPGDTAKEDAGDGTYSNSTSS 179

Db 121 FRESHCYCILVSSSEQPVYQVLAQKAVLNRCYQSVWLPGDVALKPRPEGA TMWVHA 179

QY 180 GTPVVFPDPTEAAALVEATINAKSVTLPAGKGNARAOVLELAEKIKSPPIGHALGKQY 239

Db 180 PQPVVTPEEEBLRKLAQQLRKYSSNIALMCGGCGAHHKELVEFKIKAPTVHALRK 239

QY 240 I0HENPEEVGMSGLIGYGCVIDASNEADLLILGTDYFSDLEPKD NWQAVDINGAHIG 298

Db 240 VEYDNPYDVGMGLIGFSGGFTMMNAOTLVLGTOFYRPFYPTDARIQIDINPASIG 299

QY 299 RRTVVKYPTGDAVTEILPHKEKDRFLDRMLKAHERKLSSVETTYTHNEHVLP 358

Db 300 AHSKYDMAVGLGDKRSTLRLALLPVKEKDRFLDADYR -ROARKSLDDIAPKSE -A 356

QY 359 IHPVVASLINEADKDAVFTVDTGMCNNWHARYLENPEGTRDFVGSFRGTMANALPHA 418

Db 357 IHPQYLAQOQISHFADDAITFTCVOGTPIVWAAYKL MNKRRLLGSGFNHGSMANAMPQA 415

QY 419 IGAOSVDRNQVIAAMCGGGGLGMGLGEILTVKLHQPLKAVFVNNSLGLGMVAKLEMVGE 478

Db 416 LGAQATEPERQVAMCGDGFSMMGDFLSVVMOKLPVKVIVFNNSLGLGMVAKLEMV 475

QY 479 PEQGDHEVNFIAAAGIKSVRTPKVKREQLAEALAYPGPVLIDIVDPNALISIP 538

Db 476 LTDQTELHDNPINPARTAEAGCIGTRIVEKASEDEALRAFTGSPVIVDWWAKEALAP 535

QY 539 PTITWEQWMGFSKAATRVFVGGVGAMIDLARSN 572

Db 536 PQIKLEQAKGFSLYMLRAILISGRGDEVIELAKIN 569

RESULT 3

DE2984

PY: Pyruvate dehydrogenase (cytochrome) PA5297 [imported] - Pseudomonas aeruginosa (strain

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000

C;Accession: D82984

R;Stover, C.C.; Blain, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L ; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A;Reference number: A292950

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-572 <STO>

A;Accession: D82984

A;Status: preliminary

A;Molecule type: DNA

A;Cross-references: GB:AE004942; GB:AE004091; NID:99951607; PIDN:AAG08682.1; GSPDB:GN

A;Experimental source: strain PA01

A;Gene: poxB

C;Genetics:

A;Cross-references: GB:AE004942; GB:AE004091; NID:99951607; PIDN:AAG08682.1; GSPDB:GN

A;Experimental source: strain PA01

A;Gene: poxB

Query Match 36.9%; Score 1101; DB 2; Length 572;

Best Local Similarity 40.6%; Pred. No. 1.9e-64;

Matches 226; Conservative 116; Mismatches 208; Indels 6; Gaps 4;

Qy 6 AEQOLIDLEAQWKRIVGLVGSLSNPIVDAVRQDIEWHYRNEAAFAARGAESLITGE 65
 ||:::||| :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 7 AEIWTETLEASVHRHCVGIVGSDTILHDTAIIHSOTOWHVRHEAAFAAGAESYISGR 66

Qy 66 LAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 125
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 67 LTACAGSGCPGSLHFINGVYERQRNRPMLIASQTYPQLGMEFPOEVDFKAVYASC 126

Qy 126 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 185
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 127 FCEQVHREPEQARRKVALACQAANRRCGAVVILPADIQSATVKDDL--PFSTHPQDLR 184

Qy 186 PDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 185 PSDNEQDVARYLAHKGKIGIAGSCGOGAHULLVLAADRKAINTSRADKFEDVNP 244

Qy 246 FEQMGSGLILGAGCAGCVDASNEADLLILGLTDPSDFLKP-KDNVAQDINGAHIGRTTV 304
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 245 FNGMTGMGLIESFGHMTECDTLLLGADFAWAQFPOKATLQVDRGSHLRRHPID 304

Qy 305 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 364
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 305 LGVVGVDVPTLRLPLPILAEERSRSRFLDECLRSRSLT--ERQAGKELRHQHL 362

Qy 365 ASIINELADKDAVFTVTDGMCMNWHRAYIENPFGTROEVGSFRHTMANALPHAIGQSV 424
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 363 VSLLDQIASEDRAFTAGGSAMWLLRHHS-NNGKRLTSLVHGTMANAMQALGKKA 421

Qy 425 DRNRQVIAAMCGDGCGMLGMLGELITVVKLHQPLKAVVNNSLGMVKLEMVLVCGPERCTD 484
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 422 YPERQVISGDOGLAMLGDLTTAQEKLPKVVNNLNFSNELEQKVEGLLDNYTD 481

Db 485 HEEVNFTEIAAMAGKIVSRTPPKKVREOLAAVLAQGPVLIDIVTPNAAISPPTTWE 544
 ||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 482 LIPNDFARLAEVIGFHQRKVTSSEELERAVOFRLAQGPALIDVHTPAELNMPKIEFG 541
 ||:||:||:||:||:||:||:||:||:||:||:
 Qy 545 QVNGFSKAATRVFGG 560
 ||:||:||:||:||:||:
 Db 542 QVNDTALYAAKAVLSG 557

RESULT 4

S01682 probable pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - *Pseudomonas* sp.

C;Species: *Pseudomonas* sp.

A;Variety: amylobacteriosa SB-15

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 15-Oct-1999

C;Accession: S01682

R;Ammura, A.; Fujita, M.; Futai, M.

R;Ammura, A.; Fujita, M.; Futai, M.

R;Submitted to the EMBL Data Library, November 1988

A;Description: Amino acid sequence of a protein by a region downstream of the isoamylase Escherichia coli.

A;Reference number: S01681

A;Accession: S01682

A;Molecule type: DNA

A;Residues: 1-396 <AM>

A;Cross-references: EMBL:X13378; NID:945380; PIDN:CAA31755.1; PID:945382

A;Experimental source: strain SB-15

A;Note: the source is designated as *Pseudomonas amylobacteriosa*

C;Keywords: FAD; flavoprotein; lipid binding; magnesium; membrane protein; oxidoreductase

F;51/active site: Glu #status predicted

Query Match 30.2%; Score 902.5; DB 2; Length 396;
 Best Local Similarity 49.0%; Pred. No. 1.1e-51; Matches 176; Conservative 72; Mismatches 98; Indels 13; Gaps 4;

Qy 6 AFQCLIDLEAQWKRIVGLVGSLSNPIVDAVRQDIEWHYRNEAAFAARGAESLITGE 64
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 7 ADWVTEPLHVAGKRIYGUVGQDLSNLGTDSSLRRGDDIWHRHREEAAFAAGAEARLTG 66

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 126

Qy 125 YCEMVNGEGERILHHAIAOSTMAGKVSVVLPGDIAKEDADGDTYSNSTISGGTV 184
 ||:||:||:||:||:||:||:||:
 Db 127 HYCELVSSPEQOLCVCLESATRAAVGLRQVAVVTPGDYALRESNAKAPAGASHLRLPV 186

Qy 185 FDPTEAALVAEINNAKSVTLECCAGVKNARAQVLEAKTKSPIGHALGGQYQIHENP 245
 ||:||:||:||:||:||:||:||:
 Db 187 QPAADVDAQALNDSGKVTLICRGRCAGAHDPLVLAALKAPIVHAFGKKEYVDN 246

Qy 245 PFEVGMGSLILGAGCAGCVDASNEADLLILGLTDPSDFLKRD-NVAQDINGAHIGRTTV 303
 ||:||:||:||:||:||:||:||:
 Db 247 PYDVGMTGILIGFSSGYHAMLNCITLMLGTDPSYPROFYPADAKIAQDVRPNLGRARL 306

Qy 304 KPYVTGDAVATIONILIPWKEKURSFDRMLKAWERKLSSVYTETVNEKIVPIHEYV 352
 ||:||:||:||:||:||:||:||:
 Db 307 DLGMGVGDVSATIGALLPKLKARTDRAYIDACL-AHYRKAREGIDELPPASRDASPFTN 364

Qy 65 ELAVCAASCGPGNHLIQLGGLDSHNRGAKVLTATSHPSAQISTFFOETHPELFKECS 124
 ||:||:||:||:||:||:||:||:
 Db 67 ELAVCAGSGCPGNHL

QY 354 EKHVPIRPEVVASILNEADKAVFTVDTGMCNWHRAYIENPEGTRDFVGSFRHCTMAN 413
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 403 R--PPIRQYIISVLRELDDAILTLDVGNGNWGRNFQ-MKSURGESFSQVTNGSMGF 458
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 414 ALPHATAGAQSVDRNRQVITAMCGGGGLGMLGELLTWKHLQPLKAVVFNNSIGMVKLEM 473
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 459 GLPATAAQLEPPDROVCT-----NNRNLMIMEQ 490
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 474 LVEQOERFGTHEEVFAEIAANGIKSVRITDPKVREQLAEALAYGPVPLIDIVTP 532
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 491 RVEGFPWMPOTELQDCDPAFGFENGGGLRVDPPGSELEDSFREALGTDGPVLDIDTP 549
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 RESULT 8
 R64334 acetolactate synthase (EC 4.1.3.18) large subunit - Methanococcus jannaschii
 C;Species: Methanococcus jannaschii
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 C;Accession: F64334
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Fraser, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Science 273, 1058-1073, 1996
 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A;Reference number: A64330; MUID:96337999
 A;Status: Preliminary; nucleic acid sequence not shown;
 A;Molecule type: DNA
 A;Residues: 1-591 <BBL>
 A;Cross-references: GB:U67483; CB:L7717; NID:92826270; PIDN:AAB98265.1; PID:9159103; 1
 C;Genetics:
 A;Map position: REV264626-262851
 C;Superfamily: acetolactate synthase large chain; thiamin pyrophosphate-binding domain C;Keywords: carbon-carbon lyase; oxo-acid-lyase
 C;436-484/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 19.6%; Score 586.5; DB 2; Length 591;
 Best Local Similarity 29.5%; Pred. No. 9e-31; Mismatches 166; Conservative 109; Mismatches 247; Indels 41; Gaps 16;
 Matches 16;

QY 6 AEQOLIDTLEAQVKRIVGLVGSLSNPIVDAVROSDIEWHVNRNEAAFAAGAESLTGE 65
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 4 AEAIKALEASGVKILFGPGVGAFLFYDALYSDLJHLTIRHEQAHAADGFARASGE 63
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 66 LAVCAAASCGGPNTNHIOGLYDSHRNGAKVLAIAHSITPSAQIGSTFQETHPPEILRKECSG 125
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 64 AGCVNSTSGPATNLVGTIATAVADSSPVIALTGQVPTKLIGNDAFOEIDALGLFMPITK 123
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 126 YCEMVNGEGERILHHAIQSTMAGK-GVSVVVVIEDIKEADAGDGTY--SNTISSGT 181
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 124 HNFQIKKPEEPETFRAEFLATTGPGPVHDLPLKVDQGEIDIEKYPKIPAKVDPGK 183
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 182 PVVFDPPTEAALVEINNAKSVTIFCGAGV-KNARAQVLEELAEKKIKSPIGHALGKQY 239
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 184 PKTVGHIPLQTKAALKLNESERPPVILLAGGGVITISGASEELLRLAEFVKIPVCTUNGKG 243
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 240 IQHENPEVGMSGLLGYGACVDAASNADLILLGTDIFPYSD-----FLPKDNAQVD 291
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 244 FPEPDHPLALGAWMGHTKAANYAVTCVDVLAIGCRF--SDRVTDIYAPEAKIHID 301
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 292 INGAHIGRRTTVKYKPTGVATIENILP---HVKEKTRDSFLDRMLKAHERKLSSVVETYTHVER 346
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 302 IDPAEIGKVNVRADLPVGDAKVNRLLAIALEKDK--ETWLRIVEL--KKLISIPM 357
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 347 EYTHVNEKHPHPEY---VASLNEAD--KDAVFTVDTGMCNWHRAYIENPEGTR 400
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 358 MDFDDK---PIKOPRFVKDMLEVNEIDSKLKNITTDVGONWMMAFFKT-KMPR 411
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 401 DFVGSRHRGTMANALPHATGQSVDRNRQVITAMCGDGGLGMLGELLTWKHLQPLKAVV 460
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db 412 SLASGGLTGMFGFPAAIGARVAKPVANVISITGOGFLMSQELATISYDIPWICL 471
 QY 461 FNNSLGMV-KLEMLVQGPQERGTD-HEEVNEAEIAAGIKSVRITDPKVREOLEAL 518
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 472 FDNTLGWVQMONLYQGQROSEVHGESPDFVKLAEASYVKAADRITSPDEIKEKLEAI 531
 QY 519 AYPGPVLIIDIVDP-NAL-SIPP 539
 ||| :||| :||| :||| :||| :||| :||| :|||
 Db 532 LSNEPYLIDIVDPAEALPMVPP 554
 ||| :||| :||| :||| :||| :||| :||| :|||

RESULT 9
 C69059 acetolactate synthase (EC 4.1.3.18) large chain - Methanobacterium thermoautotrophicum
 C;Species: Methanobacterium thermoautotrophicum
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
 C;Accession: C69059
 R;Smith, D.R.; Boucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadfora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; JWani, K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.; J. Bacteriol. 179, 7135-7155, 1997
 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H
 A;Reference number: A69000; MUID:98037514
 A;Accession: C69059
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-577 <MTB>
 A;Cross-references: GB:AE000666; NID:92622541; PIDN:AAB8591.1; PID:92622556
 A;Experimental source: strain Delta H
 A;Genetics:
 A;Gene: MTH1444
 A;Start codon: CGC
 C;Supercategory: acetolactate synthase large chain; thiamin Pyrophosphate-binding domain C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein F;428-476/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 19.3%; Score 576; DB 2; Length 577;
 Best Local Similarity 26.8%; Pred. No. 4 2e-30;
 Matches 149; Conservative 117; Mismatches 267; Indels 24; Gaps 9;
 QY 7 EQOLIDTLEAQVKRIVGLVGSLSNPIVDAVROSDIEWHVNRNEAAFAAGAESLTGE 66
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 8 QAIIRSLLDQGADTVFQGPQGLPLVDMYDSELKRHLVRLHEOCAHADGYARASGRV 67
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 67 AVCAASCGGPNTNHIOGLYDSHRNGAKVLAIAHSITPSAQIGSTFQETHPPEILRKECSG 126
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 68 GVCIAATSGGGPATNLVNGIATAMNDAPSIVATAQVOPHILGNAFOEYDVGIMTPIKTH 127
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 127 CEMVNGEGERILHHAIQSTMAGK-GVSVVVVIJDIAKEDADGDTYSNSTISSGPWF 185
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 128 SFQPSDASEIPIAVRASFHFKTGRCPGPVWLPLKIQEELME-BVDDLELPGRPNK 186
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 186 PDPTTEAAALVEINNAKSVTIFCGAGV-KNARAQVLEELAEKKIKSPIGHALGKQYTOHE 243
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 187 GHPLQTKRAEIJRRSKPKVILLAGGGVITISGASREIKELSDLIKAVPTTTLGKGSFPE 246
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 244 NPFEVENSGLGLGYGACVDAASNADLILLGTDIFPYSD-----VSDELEKDNVQDINGAII 297
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 247 HPSAMGMUGMIGRKVANLVTBCDCJLAVAGGRFSDRITGNGYAFAAARNITHVDDPAA 306
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 298 GRRTVKYKPTGVATIENILP-EKTDRSFLDRMLKAHERKLSSVVETYTHVER 355
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 307 GKNVGVYDPTVGDARNVLRLEJIAKLYKKEQSWSQRER-----ADCMRPMSYD 359
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 QY 356 HVPTHPEV VASILNEADKAVFTVDTGMCNWHRAYIENPEGTRDFVGSFRHCTMAN 415
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 360 EVPLKPOQVKEISQVADDETWTVDQONWMMAFFYTS-RAPRKFTISGGLGTMGFG 418
 ||| :||| :||| :||| :||| :||| :||| :|||
 QY 416 PHAIGOSVDRNRQVITAMCGDGGLGMLGELLTWKHLQPLKAVVFNNSIGMVKLEMV 475
 ||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 419 PAAGKVALPDSWAVCGDGGLFLAVQDIAIREYDIPVICIMDRNHRGMVQWRL 478
 ||| :||| :||| :||| :||| :||| :||| :|||

Db	482	YDIQVKTITLNINGWGMVRQWQTFYEERYASNSMSQMP-----DINL--LCEAYGI	533
Db	479	FYDERMSIHTHLGEVDPDFVKLAESFGVEAERIEPGETSEALSRAIRSGEPALLDIVIDP	538
Qy	534	AL--SIPPTITWEQMG 548	
Db	539	EILPMVPPGCGLTLTEIVG 555	
RESULT	10		
S75115		B69644	
acetoxyacid synthase - Synechocystis sp. (strain PCC 6803)		acetolactate synthase (EC 4.1.3.18) large chain - Bacillus subtilis	
N; Alternate names: protein slr2088		C; Species: <i>Bacillus subtilis</i>	
C; Species: <i>Synechocystis</i> sp.		C; Accession: B69644, 139865	
A; Variety: PCC 6803		C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000	
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000		C; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber	
C; Accession: S75115		C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capriano, V.; Carter, N.M.;	
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;		A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,	
O.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda		Nature 390, 249-256, 1997	
DNA Res. 3, 109-136, 1995		A; Authors: Fouger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gal	
A; Title: Sequencing analysis of the genome of the unicellular cyanobacterium <i>Synechocystis</i>		iach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hu, M.; Koettler, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Laredo	
S.; Reference number: S74322; MUID:97061201		Y.; M.; Ogawa, K.; Ogihara, A.; Oludega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete	
A; Accession: S75115		Rieder, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scarl	
A; Status: nucleic acid sequence not shown; translation not shown		Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya	
A; Molecule type: DNA		T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasuda, Y.; Yata, K.; Yoshida	
A; Residues: 1-621 <KAN>		A; Authors: Yoshikawa, H.F.; Zamstein, E.; Yoshikawa, H.; Danchin, A.	
A; Cross-references: EMBL:D90910; GB:AB001339; NID:9162956; PIDN:BAA17977_1; PID:9165306		A; Title: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtili</i>	
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996		A; Reference number: A65580; MUID:9804403	
C; Genetics:		A; Accession: B69644	
A; Gene: ilvG		A; Status: preliminary; nucleic acid sequence not shown; translation not shown	
A; Start codon: GTG		A; Molecule type: DNA	
C; Superfamily: acetolactate synthase large chain: thiamin pyrophosphate-binding domain		A; Residues: 1-574 <RUN>	
Query Match	19.0%	Best Local Similarity	27.4%
Matches	164	Score	567
Local	Conservative	DB	2
Matches	113	Length	621
Mismatches	236	Pred. No.	1.8e-29
Indels	86	Gaps	18
Db	9	Qy	LIDTLEFAQVKRIGVINGSLNPVDAVRO---SDIEWHVRNEAAFAAGAEGLSTG 64
Db	27	Qy	LMDSLKURHGKVHKIGPGGAKLPLPYDELRFEAEGEIELHVRMEQGASHADGQARATG 86
Db	65	Qy	ELVACAASCAGPGNTHIQLQGDYDSHRNGAKVLAISHTPSAQIGSTFFOE-----THPEI 118
Db	87	Qy	KVGWCFGTSGFGAQNLTVGIANAHLDHSVKNVWITGVQVGRAMIGSDAQFOIDIFGTLPLV 146
Db	119	Qy	LFKECSGYCMVNNGEQGEQEIILHAIQSTMAGK-GVSVVWPGDIAKE-----DAGDG 170
Db	147	Qy	----KHSYVSRADMARIVTAHFHLASTGRGPVLIDPKVGLVSECEYIFLPDG- 199
Db	171	Qy	TYSNSTISSTPVPFPDPEAAVLYEAVINNAKSTLFCGGC- VKNARAQVLEAKITS 228
Db	200	Qy	----VNLPGYRPTVKGPNRQINAALQLEQARNPLWYGGATAANAHQAQVQEAEQL 255
Db	229	Qy	PIGHALGGKQYIQHENPFVEGMSCSLLGQYACVDSASNEADDLTLIGTDF-----PYSDFL 282
Db	256	Qy	PTVTILMIGAFDHNPLSVMGLMHGHTAYANFAVSECIDLAVGARFDDRVTKGLDEFA 315
Db	283	Qy	PKDWAQVQDINGAIGRRTVVKPVTVGAAATENILHVK-----KTDRLFLORML 335
Db	316	Qy	3RAVKVHTIDPVAVGKNRAPDVPIVGDRVHLFQLLORARELDPYTHPTHQAWLNRL- 373
Db	336	Qy	KAHERKLSSVYETVTHNVEKINVTPHEYYA- STLINEADK--DAVFVTDGMCNVWHAR 391
Db	374	Qy	-----IDHRTTDYPLQVPHYEDTIAQPQEWVHETGRQADPAVYITDVQOHQWRAQ 423
Db	392	Qy	392 YIENPEGTRDFVGSSFRHGTMANALPHAQASVDRNRQVIAMCGGGLGMLGFILVNL 451
Db	424	Qy	FLNN--GPRRIWSSAGLGLTMGFLGLPAMGAKVGVGDEAVICISGDAFQMNQLQELGTLAQ 481
Qy	452	Qy	452 HQPLKAVVENNSSLGMK-----LEMVLEQPERCTDHEEVNFALAAAGI 499
RESULT	11		
B69644		acetolactate synthase (EC 4.1.3.18) large chain - <i>Bacillus subtilis</i>	
C; Species: <i>Bacillus subtilis</i>		C; Species: <i>Bacillus subtilis</i>	
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000		C; Accession: B69644, 139865	
C; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber		C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000	
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capriano, V.; Carter, N.M.;		C; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber	
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,		C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capriano, V.; Carter, N.M.;	
Nature 390, 249-256, 1997		C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000	
A; Authors: Fouger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gal		A; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber	
iach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hu, M.; Koettler, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Laredo		C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capriano, V.; Carter, N.M.;	
Y.; M.; Ogawa, K.; Ogihara, A.; Oludega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete		A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,	
Rieder, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scarl		Nature 390, 249-256, 1997	
Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya		A; Authors: Fouger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gal	
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasuda, Y.; Yata, K.; Yoshida		iach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hu, M.; Koettler, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Laredo	
A; Authors: Yoshikawa, H.F.; Zamstein, E.; Yoshikawa, H.; Danchin, A.		Y.; M.; Ogawa, K.; Ogihara, A.; Oludega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete	
A; Title: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtili</i>		Rieder, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scarl	
A; Reference number: A65580; MUID:9804403		Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya	
A; Accession: B69644		T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasuda, Y.; Yata, K.; Yoshida	
A; Status: preliminary; nucleic acid sequence not shown; translation not shown		A; Authors: Yoshikawa, H.F.; Zamstein, E.; Yoshikawa, H.; Danchin, A.	
A; Molecule type: DNA		A; Title: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtili</i>	
A; Residues: 1-574 <RUN>		A; Reference number: A65580; MUID:9804403	
A; Cross-references: GB:Z99118; GB:AL009126; NID:92635200; PIDN:CAB14791_1; PID:926352		A; Accession: B69644	
A; Experimental source: strain 168		A; Status: preliminary; nucleic acid sequence not shown; translation not shown	
R; Grandori, J.A.; Zahler, S.A.; Calvo, J.M.		A; Molecule type: DNA	
J. Bacteriol. 174, 3212-3219, 1992		A; Residues: 1-20, 'R' <RES>	
A; Title: transcriptional regulation of the ilv-leu operon of <i>Bacillus subtilis</i> .		A; Cross-references: GB:M87009; NID:9143096; PIDN:AAA22550_1; PID:9143097	
A; Reference number: I39865; MUID:92250415		A; Genetics:	
A; Status: preliminary; translated from GB/EMBL/DDJB		A; Gene: ilvB	
A; Molecule type: DNA		C; Superfamily: acetolactate synthase large chain: thiamin pyrophosphate-binding domain	
A; Residues: 1-20, 'R' <RES>		C; Key words: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; F; 64/Active site: Glu #status predicted	
A; Cross-references: GB:M87009; NID:9143096; PIDN:AAA22550_1; PID:9143097		F; 64/Active site: Glu #status predicted	
A; Genetics:			
Query Match	18.6%	Best Local Similarity	28.7%
Matches	154	Score	554.5
Local	Conservative	DB	2
Matches	113	Length	574
Mismatches	251	Pred. No.	1.1e-28
Indels	19	Gaps	9
Db	4	Qy	SRAQDLITLEFAQVKRIGVNGLWDSDLNPVDAVQRQSDIEWHVRNEAAATAGATSLIT 63
Db	19	Qy	SGALMIESLKKEVEMIFGVGPGVAPIKLYNSLVLHPRHOGAITHAEGYARVS 78
Db	64	Qy	GELAVCAASCGCPNTLHQGLDLSHRSRNGAKVIAISHTPSAQIGSTFFOEHTPEI 123
Db	79	Qy	GKPGWVIASTSPGATNLVTLGADAMIDSPLVWFTGQVATSVIGSDAQEADLGLITMPV 138
Db	124	Qy	SGCCEMINGGEGGERILHAIQSTMAGK-GVSVVWPGDIKEADGDTGSNSTISSG-T 181
Db	139	Qy	TKSYQVQRPEDLPRIKEAFLATTGRGPVPLIDIPKDVTIE-GEFSYHEMLNPLGYQ 197
Db	182	Qy	PVFPDPDEAALVEATNNAKSYTFLFGAGVNARA-QVIELAEKIKSPHTGAHGGKQY 239
Db	198	Qy	PTEPNUFLQIRKIVEAVSSAKRPPVILAGAGYUHGKASEELKINYAQOQIPWAHTLGLGG 257
Db	240	Qy	TOHENPFEVGMSGILGSGYACVDSASNEADLILLGTDPP-VSDFLIPDNVAQVDIN 293

RESULT 12

T11997 acetohydroxyacid synthase large subunit - red alga (Cyanidium caldarum) chloroplast
 C;Species: chloroplast Cyanidium caldarum
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-May-2000
 C;Accession: T11997
 R;Gloeckner, G.; Rosenthal, A.; Valentin, K.
 submitted to the EMBL Data Library, September 1997
 A;Description: Organization of 46 kb of the Cyanidium caldarum RKL plastid genome.
 A;Reference number: Z17374
 A;Accession: T11997
 A;Status: preliminary; translated from GB/EMBL/DBDJ
 A;Residue: 1-585 <GLO>
 A;Cross-references: EMBL:AF022186; NID:92465730; PIDN:AAB82660.1; PID:92465731
 A;Experimental source: strain RKL
 C;Genetics:
 A;Genome: chloroplast
 A;Note: 1IVB
 C;Superfamily: acetolactate synthase large chain; thiamin pyrophosphate-binding domain
 C;Keywords: chloroplast
 F:446-494/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 18.4% Score 549; DB 2; Length 585;
 Best Local Similarity 27.3%; Pred. No. 2.5e-28;
 Matches 160; Conservative 112; Mismatches 247; Indels 68; Gaps 15;

Qy 9 LITTLEAQVKRIGVYDSDLNPVIDAV---RQSDIEWHVRNEEAFAAGAESLITG 64
 Db 16 LIDMLVKHKVKFNFGVPGGLPILYDELYWERKKLKHVLRHEQSAAHAYARATN 75
 Qy 65 ELAVCAAASCGPGNTHILOGLYSHRNAGKVALNHSHTPSAOGISTFFOET- 124
 Db 76 EVGVCLATSGPATNLVFGIATAQMDSPVPIAITGQVSRAFICIDAQEVDFGIFTPLIV 135
 Qy 125 GYCENMVNGEGERILHIAIQSTMAGK-GVSVVVIPGDIAKEDAG---DGTVSNSTIS 179
 Db 136 KHSFVVRDPDRDISTIVSEAFYISKHGRPAVLLDVPKDVGLEEFNYHDYDSRDHKPIT 195
 Qy 180 GPPVVFDPTEAALVEINANNAKSVTLECCAGAGVKNARQ--VLEAEKIKSPIGHALGGK 237
 Db 196 YRPIGYISRIQEKFKMLKEKOPILYVGGGVMSRQHETEELASFKIPVITLNGK 255
 Qy 238 QYIQHENPFEVMSGGLGYYGACVDAHSNDLILLGDF----PYSDFLPKDNVAQWD 291
 Db 256 GSFNEYNNPLYLGMGMHTAYANFANSCECDLTLGARFDDRTGKUDFACQAQVHTWD 315
 Qy 292 INGAUHRRRTVVKPVNGDWAINTILPHVKEKTDRLMKAHERKLSSWVETH 351
 Db 316 IDPAAEIGKRIPOLAIISDIKIVKELLSSMKGTNN--MDK-----NOTQAWHL 363
 Qy 352 NVEK-----HVP-----IHPYVASLNLADKDAVFTVDTGMCNNWHARYVIENPEGT 399

RESULT 13

A44857 acetolactate synthase (EC 4.1.3.18) - Spirulina platensis
 C;Species: Spirulina platensis
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 15-Oct-1999
 C;Accession: A44857
 R;Milano, A.; De Rossi, E.; Zanaria, E.; Barbierato, L.; Ciferri, O.; Riccardi, J.; Gen. Microbiol. 138, 1399-1408, 1992
 A;Title: Molecular characterization of the genes encoding acetohydroxy acid synthase
 A;Reference number: A44857; MJD:92381487
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-612 <ML>
 A;Note: sequence extracted from NCBI backbone (NCBIn:112275, NCBIP:112276)
 C;Superfamily: acetolactate synthase large chain; thiamin pyrophosphate-binding domain
 C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; oxo-acid lyase
 F:446-494/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 18.3% Score 546; DB 2; Length 612;
 Best Local Similarity 26.6%; Pred. No. 4.2e-28;
 Matches 164; Conservative 123; Mismatches 253; Indels 76; Gaps 19;

Qy 6 AEQLDTTLEAQVKRIGVYDSDLNPVIDAV---AVRQSDIEWHVRNEEAFAAGAESL 61
 Db 15 AFLRDLISKKRIGVQIIFGPYPOGAIUPIDYELRAREEGDQIQLHVRHEQGASHADGYAR 74
 Qy 62 ITGELAVCAASCGPENTHILQGLYSHRNAGKVALNHSHTPSAOGISTFFOET---- 114
 Db 75 ATGRVGVGCFGTSGPATNLVFGIATAHMDSPTPMVITQVARPAIGTDAQDSDFGILT 134
 Qy 115 ---HPEILKECSGCGYCEMMNGGECE--RILHHAQIQTSMAGK-GVSVVVIPGDIAKED- 166
 Db 135 PIVKHSYV-----REFGDMARIAVAFHIASTGRGPSPVLFIDVPKDVGLEEF 181
 Qy 167 ---AGDGTYSNSTSSGTPVVFPPTEAALVEINANNAKSVTLCGAGY--KNRAOVL 220
 Db 182 DYIPPNPGEVS--LPGYPRVKGWRQIMQAIKLEEEAERPLMMVGGATSATMAREIA 238
 Qy 221 ELEAKIKSPIGHALGGKQYIOPENPEVGMGSLGLGYYGACVDAHSNDLILLGDF--- 276
 Db 239 EAEFLFOIPTVTTGKSFDEKHLPSLVGMGMHOTAYANFAVSCDFLTAVGARFDDRV 298
 Qy 277 --PYSDFLPKDNVAQWDINGAHHGRTPTVVKPVGTDVAAATTILPHVKEKID---- 327
 Db 299 TGKLDDEFGSRAKVHIDIDPAEVGNRTPPEVGDYVROLHLRRCREIGDVGNDQT 358
 Qy 328 RSFLRMLKAHERKKSWSWVETHVKVPHPEVWASTLNELADKDAVFTVDTGMCNV 387
 Db 359 OSWLWIRNRAPE-DPLVWVSYSDS-----LSPOVIAEIGKMA-PDGVYPTDQHOM 410
 Qy 388 WHARYTENPECTRDVGSFRHGTMANALPHAIGAOSVDRNRQVIAAMCGDGLGMLGELL 447
 Db 411 WAQFLKN- GPROQNTSAGIGTMYGIAPSAGAVALERSQVCIAGTAGDASVQMINQEL 468
 Qy 448 TVKLRQPLKAVVNNSLGMVKLMLVQEPEFSIDHVEY--IPEATAAAGIKSVRI 504

Db	469	TIAQYGINVKTVLNINGWGMVYMRQWQQRFGYERYSASNMIGMDFEMLARSYGVKGMV	528	Db	475	TINNAVLGMYRQWQQLFYDKRYSEVDLSQPPD-----FVKLAEMAGAVGMRAKKP	525
Qy	505	TDPKKVREQLAELAYFGPVNLID--IVTPPNAL-SIPTITWQMWS---KAATR	556	Qy	509	KVREGDLAEALAYPG-PVLLDIVTD--PNAISIPP	539
Db	529	KSRDELHQALAEMLAYDGPVLMVHVTKDCEYPMVAPGRSNQMICPERROLEKAVEL	588	Db	526	EVREVIIEARKIDDPRVILFDWVDEENVLPMPV	559
Qy	557	VFGGGVAMIDARSN	572				
Db	589	IYCSNCGAK-NVASNN	603				
RESULT 14							
C70341		acetolactate synthase (EC 4.1.3.18) large chain - Aquifex aeolicus		C;Species: chloroplast Porphyra umbilicalis (laver)			
C;Species: Aquifex aeolicus				C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Oct-1999			
C;Accession: 08-May-1998 #sequence_revision 08-May-1998 #text_change 15-Oct-1999				C;Accession: S28920; S27402			
C;Accession: C70341				R;Reith, M.; Monholland, J.			
R;Becker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ow				Curr. Genet. 23, 59-65, 1993			
V.; Nature 392, 353-358, 1998				A;Title: Two amino-acid biosynthetic genes are encoded on the plastid genome of the r			
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.				A;Reference number: S28920; MUID:93153832			
A;Accession: C70341				A;Accession: S28920			
A;Status: preliminary; nucleic acid sequence not shown; translation not shown				A;Molecule type: DNA			
A;Molecule type: DNA				A;Residues: 1-590 <REI>			
A;Residues: 1-585 <ACD>				A;Cross-references: EMBL:M94625; NID:9343129; PIDN:AAA03052.1; PID:9343130			
A;Cross-references: GB:AE000690; NID:92983100; PIDN: AAC06706.1; PID:92983101; GB:AE00065				C;Genetics:			
A;Experimental source: strain VF5				A;Gene: llVB			
C;Genetics:				C;Superfamily: acetolactate synthase large chain; thiamin pyrophosphate-binding domain			
A;Gene: llVB				C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; m			
C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; m				F;44-488/Domain: thiamin pyrophosphate-binding domain homology <TPB>			
F;44-488/Domain: thiamin pyrophosphate-binding domain homology <TPB>							
RESULT 15							
Qy	528920	acetolactate synthase (EC 4.1.3.18) - red alga (Porphyra umbilicalis) chloroplast		C;Species: chloroplast Porphyra umbilicalis (laver)			
Db	528920	acetolactate synthase (EC 4.1.3.18) - red alga (Porphyra umbilicalis) chloroplast		C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Oct-1999			
Qy	509	KVREGDLAEALAYPG-PVLLDIVTD--PNAISIPP	539	C;Accession: S28920; S27402			
Db	526	EVREVIIEARKIDDPRVILFDWVDEENVLPMPV	559	R;Reith, M.; Monholland, J.			
RESULT 15							
Qy	9	LIDTTEAQSYKRTGYGLVGSLNPLIVDAV---RQSDIENHVNRNEAAFAAGAESLITG	64	C;Species: chloroplast Porphyra umbilicalis (laver)			
Db	17	LIDSTVRGHYIHTINGYQGGAIRPLATEWEEELSLSKNIYLVRHOGASHAADYWSRSTG	76	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Oct-1999			
Qy	65	ELAVCAASCGPNTLHQIQLGDHSRNGAKVLAISHAHSQPSAQIGSTFFQETHPEILFKECS	124	C;Accession: S28920; S27402			
Db	77	KVGVMVMTSGPATNLVTPIDADMVSVPVLAITGQYPTHLIGNDFOEQDVIGTRPIT	126	R;Reith, M.; Monholland, J.			
Qy	125	GYCENVNNGGEQGERILHHAJQSTMAGK-GVSVVVIPGDIAKEDADGDTYSNSTISSTG	183	Curr. Genet. 23, 59-65, 1993			
Db	137	KHSVYVVRDPRDSRIVAAFYICKRGPGPVLDPKDVGLE----KFNFSVEPGQV	191	A;Title: Two amino-acid biosynthetic genes are encoded on the plastid genome of the r			
Qy	181	---TPVVPDPDTAAALVAEINNAKSVLFCGAGG--VNNARAQVLEAEKISPPIGHAL	234	A;Reference number: S28920; MUID:93153832			
Db	192	IPGCRPLSNLKSRLIMAKMIDQSOSQPLYISGGAISDASHTIKELWDLYKIVTTL	251	A;Accession: S28920			
Qy	235	GGKQYIHOHNPFENGMGLIGYGACVADASNEADLILIGLDF----PYSDFLPKDNA	288	A;Cross-references: EMBL:M94625; NID:9343129; PIDN:AAA03052.1; PID:9343130			
Db	252	MKGKFNFNESEFCLGMLGMHGHTAVANFANFSECDLIALGARFDDRTVGKULDEFACNAQVI	311	C;Genetics:			
Qy	289	QVDINGAHIGRRRTWVYPVTDWVATIEMILPHVREKTDURSLLRMKHERKLSSVWT	348	A;Gene: llVB			
Db	312	HVDIDPAEVGKNRIFTQVAIVGVDTEEVTSILNLKNNF-KPYPEQQISWQER-IHRWRQ	369	C;Superfamily: acetolactate synthase large chain; thiamin pyrophosphate-binding domain			
Qy	349	YTHW-EKHPHIREYVYASILNEADKDAVFTVDTGMCNWHRAYIENPEGTRFVGSR	407	C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; m			
Db	370	YPLIVPKTSISQELVITVQNL-QDAYFTVQHOMWSAQFLK--VKSNIWSS	426	F;44-492/Domain: thiamin pyrophosphate-binding domain homology <TPB>			
Qy	408	HGTMANALPHAIGQSVDRNRQVAMCGGGGLMIGELITVKLHQPLKAVVNNSLG	467	C;Accession: S28920; S27402			
Db	427	LGTMGYGLPAAGQVAHNELVICVSGDSSFQMNQELGIATQYKLPKIVINRNWQ	474	R;Reith, M.; Monholland, J.			
Qy	516	EVAFKIDPRVILFDWVDEENVLPMPV	559	Curr. Genet. 23, 59-65, 1993			
Db	538	DAMKYPPVLDLCOVTCENYCWAWSNQAMIGLPERROLEKAVEL	576	A;Title: Two amino-acid biosynthetic genes are encoded on the plastid genome of the r			
Qy	400	RDFVGFSRHTMANALPHAIGQSVDRNRQVAMCGGGGLMIGELITVKLHQPLKAVVNNSLG	537	A;Reference number: S28920; MUID:93153832			
Db	415	ROFINSSGLGTMFGELPAGIGAKIGRPDRREVWVWDGFSVMTMQVITAQYKVPKV	577	A;Accession: S28920			
Qy	460	VFNNSLIGMVK-----LEMIVEGQEPFGTDEHEVNFAAATAAGIKSVRITDPKWR	508	A;Cross-references: EMBL:M94625; NID:9343129; PIDN:AAA03052.1; PID:9343130			

Mon Mar 19 12:21:50 2001

us-09-456-306-2.rpr

Search completed: March 17, 2001, 21:53:40
Job time: 2596 sec

*This Page Blank (Leave
Blank)*